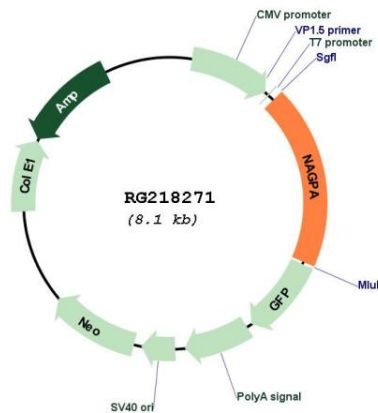


OTI Disclaimer:	The molecular sequence of this clone aligns with the gene accession number as a point of reference only. However, individual transcript sequences of the same gene can differ through naturally occurring variations (e.g. polymorphisms), each with its own valid existence. This clone is substantially in agreement with the reference, but a complete review of all prevailing variants is recommended prior to use. More info
OTI Annotation:	This clone was engineered to express the complete ORF with an expression tag. Expression varies depending on the nature of the gene.
Components:	The ORF clone is ion-exchange column purified and shipped in a 2D barcoded Matrix tube containing 10ug of transfection-ready, dried plasmid DNA (reconstitute with 100 ul of water).
Reconstitution Method:	1. Centrifuge at 5,000xg for 5min. 2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA. 3. Close the tube and incubate for 10 minutes at room temperature. 4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom. 5. Store the suspended plasmid at -20°C. The DNA is stable for at least one year from date of shipping when stored at -20°C.
Note:	Plasmids are not sterile. For experiments where strict sterility is required, filtration with 0.22um filter is required.
RefSeq:	NM_016256.4
RefSeq Size:	2219 bp
RefSeq ORF:	1548 bp
Locus ID:	51172
UniProt ID:	Q9UK23
Cytogenetics:	16p13.3
Domains:	EGF
Protein Families:	Transmembrane
Protein Pathways:	Lysosome

Gene Summary:

Hydrolases are transported to lysosomes after binding to mannose 6-phosphate receptors in the trans-Golgi network. This gene encodes the enzyme that catalyzes the second step in the formation of the mannose 6-phosphate recognition marker on lysosomal hydrolases. Commonly known as 'uncovering enzyme' or UCE, this enzyme removes N-acetyl-D-glucosamine (GlcNAc) residues from GlcNAc-alpha-P-mannose moieties and thereby produces the recognition marker. The encoded preproprotein is proteolytically processed by furin to generate the mature enzyme, a homotetramer of two disulfide-linked homodimers. Mutations in this gene are associated with developmental stuttering in human patients. [provided by RefSeq, Oct 2015]

Product images:



Circular map for RG218271